

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 21, 2001, 12:06:13 ; Search time 16.04 Seconds  
(without alignments)  
1491.198 Million cell updates/sec

Title: US-09-486-334-2  
Perfect score: 1641  
Sequence: 1 MATCIDTCRTGNTQDDSRF.....IPCLTMDQTSYLTMSDYVI 314

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR-68: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1641	100.0	314	2	S67482
2	1611	98.2	314	2	S71181
3	1215	74.0	391	2	S63192
4	1105	67.3	303	2	S68469
5	877	53.4	347	2	T09140
6	869	51.0	294	2	A57478
7	849.5	53.8	312	2	S71207
8	699	42.6	315	2	F84554
9	649.5	39.6	272	2	C81184
10	648.5	39.5	273	1	XIECSA
11	648.5	39.5	273	2	S29568
12	648.5	39.5	273	2	F86036
13	647.5	39.5	273	2	G82049
14	643	39.2	308	2	T08867
15	624.5	38.1	267	2	G64080
16	587.5	35.8	299	2	T04669
17	573.5	34.9	274	2	A84936
18	549.5	33.5	261	1	JC1293
19	472.5	28.8	270	2	T50058
20	442	26.9	225	1	E53402
21	424	25.8	217	1	B53402
22	422.5	25.7	227	1	T44913
23	420.5	25.6	249	1	S75606
24	409	24.9	251	2	T44279
25	405	24.7	229	2	H70660
26	395	24.1	229	2	F83663
27	392	23.9	258	2	A83169
28	389.5	23.7	199	2	E86856
29	388.5	23.7	212	2	C81347

30	369.5	22.5	269	1	D43706	serine O-acetyl
31	365	22.2	171	1	B64671	serine O-acetyl
32	359	21.9	171	2	B71845	serine O-acetyl
33	338.5	20.6	220	2	G72349	serine acetyl
34	312	19.0	171	2	D84302	serine acetyl
35	287	17.5	319	2	S55322	serp protein - Syn
36	265	16.1	231	2	H83381	probable acetyl
37	217	13.2	162	2	A64972	probable acetyl
38	217	13.2	162	2	B85832	serine acetyl
39	207	12.6	184	2	C82264	serine acetyl
40	179	10.9	256	2	A86660	serine acetyl
41	177.5	10.8	143	2	G82264	serine acetyl
42	175	10.7	236	2	H72245	2,3,4,5-tetrahydro
43	175	10.7	240	2	B83983	tetrahypodipicoli
44	171	10.4	201	2	H85806	hypothetical prote
45	164.5	10.0	190	2	S07000	modulation protein

## ALIGNMENTS

RESULT 1  
S67482  
serine O-acetyltransferase (EC 2.3.1.30), cytosolic - Arabidopsis thaliana  
N:Alternate names: serine acetyltransferase  
C:Species: Arabidopsis thaliana (mouse ear cress)  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 05-May-2000  
C:Accession: S67482; S52150  
R:Ruffet, M.L.; Lebrun, M.; Droux, M.; Douce, R.  
Eur. J. Biochem. 227, 500-509, 1995  
A:Title: Subcellular distribution of serine acetyltransferase from Pisum sativum and  
A:Reference number: S67482; MID:95154333  
A:Accession: S67482  
A:Molecule type: DNA  
A:Residues: 1-314 <RUF>  
A:Cross-references: EMBL:Z34888; NID:9608676; PIDN:TA84371.1; PID:9608677  
A:Note: the authors translated the codon ACC for residue 158 as Ile and ACA for resid  
C:Superfamily: serine acetyltransferase; serine acetyltransferase homology  
C:Keywords: acyltransferase; coenzyme A; cysteine biosynthesis  
F:123-283/Domain: serine acetyltransferase homology <SAT>

Query Match	Best Local Similarity	Score	DB ?	Length	314:
Matches 314: Conservative	0: Mismatches	0: Indels	0: Gaps	0:	
QY 1	MATCIDTCRTGNTQDDSRFCCIKNFRPGFSVNRKIHHTQIEDDDVWIKMLEAKSDV	60			
DB 1	MATCIDTCRTGNTQDDSRFCCIKNFRPGFSVNRKIHHTQIEDDDVWIKMLEAKSDV	60			
QY 61	KQEPILSNVYASITSHRSLSALAHILSVKLSNMLPSNT_FELFISYLESPETTEST	120			
DB 61	KQEPILSNVYASITSHRSLSALAHILSVKLSNMLPSNT_FELFISYLESPETTEST	120			
QY 121	KODLAVKRPDPACISYVHCFGLGFGFLACQAHRIATHLQKONKIYALLIQNRVSESA	180			
DB 121	KODLIVKRPDPACISYVHCFGLGFGFLACQAHRIATHLQKONKIYALLIQNRVSESA	180			
QY 181	VDHHPKAKIGKGLDHAATGAVIGETAVVGDVSLHGVLTGTGKSGGRHRIQDGYL	240			
DB 181	VDHHPKAKIGKGLDHAATGAVIGETAVVGDVSLHGVLTGTGKSGGRHRIQDGYL	240			
QY 241	IGAGSCILGNTTIGEGAKIGSGSVYKVPATTAVGNPRLIGGKPNRKHKIPCLTM	300			
DB 241	IGAGSCILGNTTIGEGAKIGSGSVYKVPATTAVGNPRLIGGKPNRKHKIPCLTM	300			
QY 301	DQTSYLTMSDYVI 314				
DB 301	DQTSYLTMSDYVI 314				
RESULT 2					
S71181					

serine O-acetyltransferase (EC 2.3.1.30) SAT precursor, chloroplast - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 05-May-2000  
 C:Accession: S71181  
 R:Murillo, M.; Foglia, R.; Diller, A.; Leustek, T.  
 Submitted to the EMBL Data Library, August 1995  
 A:Description: Analysis of a cDNA encoding serine acetyltransferase from Arabidopsis thaliana of Escherichia coli.  
 A:Reference number: S71181  
 A:Accession: S71181  
 A:Molecule type: mRNA  
 A:Residues: 1-314 <MUR>  
 A:Cross-references: EMBL:LA2212; NID:9926938; PIDN:AAC37474.1; PID:9926939  
 A:Note: probably chloroplast isoform; no transit peptide given  
 C:Genetics:  
 A:Superfamily: serine acetyltransferase; serine acetyltransferase homology  
 C:Keywords: acyltransferase; chloroplast; coenzyme A; cysteine biosynthesis  
 F:123-283/Domain: serine acetyltransferase homology <SAT>

Query Match 98.2%; Score 1611; DB 2; Length 314;  
 Best Local Similarity 98.1%; Pred. No. 2.7e-126;  
 Matches 308; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MATCIDRCRGNTODDSRRCCKNFPRGFSVNRKIHTHTQIEDDDVWIKMLEAKSDV 60
Db 1 MATCIDRCRGNTODDSRRCCKNFPRGFSVNRKIHTHTQIEDDDVWIKMLEAKSDV 60
QY 61 KOEPIISNYVYASTSHRSLESALHILSVKLSNLTNPNTLFEPLFVLESPETIEST 120
Db 61 KOEPIISNYVYASTSHRSLESALHILSVKLSNLTNPNTLFEPLFVLESPETIEST 120
QY 121 KODLIWVKERDPACISYVHCFGLFKAQAHRIAHITLTKONRKRIYALLIONRVSSEA 180
Db 121 KODLIWVKERDPACISYVHCFGLFKAQAHRIAHITLTKONRKRIYALLIONRVSSEA 180
QY 181 VDIHPGAKIGKGIILDHATGVVIGFAVGVNDVSTLHCVTLGGTGKSGDRHPRKIGDVL 240
Db 181 VDIHPGAKIGKGIILDHATGVVIGFAVGVNDVSTLHCVTLGGTGKSGDRHPRKIGDVL 240
QY 241 IGAGSIIIGNITIGGAKIGSGSVVVKDVPARTTAVGNPARLIGKKNPKRKHDPICLT 300
Db 241 IGAGSIIIGNITIGGAKIGSGSVVVKDVPARTTAVGNPARLIGKKNPKRKHDPICLT 300
QY 301 DOTSYLTEMSDYVI 314
Db 301 DOTSYLTEMSDYVI 314

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RESULT 3 S69192

serine O-acetyltransferase (EC 2.3.1.30) SAT-1a precursor, chloroplast - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 05-Dec-1996 #sequence\_revision 27-Feb-1997 #text\_change 05-May-2000  
 C:Accession: S69192; S71906  
 R:Roberts, M.A.; Wray, J.L.  
 Plant Mol. Biol. 30, 1041-1049, 1996  
 A:Title: Cloning and characterization of an Arabidopsis thaliana cDNA clone encoding an

A:Reference number: S69192; MUID:96270381  
 A:Accession: S69192  
 A:Molecule type: mRNA  
 A:Residues: 1-391 <ROB>  
 A:Cross-references: EMBL:U22964; NID:q1184047; PIDN:AA807778.1; PID:q1184048  
 R:Hell, R.  
 Submitted to the EMBL Data Library, July 1995  
 A:Reference number: S71906  
 A:Accession: S71906  
 A:Molecule type: mRNA  
 A:Residues: 80-391 <HEL>  
 A:Cross-references: EMBL:X82888; NID:9897677; PIDN:CAA58061.1; PID:9897678  
 C:Genetics:  
 A:genome: nuclear

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology  
 C:Keywords: acyltransferase; chloroplast; coenzyme A; cysteine biosynthesis  
 F:1-60/Domain: transit peptide (chloroplast) #status predicted <TRP>  
 F:61-391/Product: serine O-acetyltransferase SAT-1a, chloroplast #status predicted <M>  
 F:200-360/Domain: serine acetyltransferase homology <SAT>

Query Match 74.0%; Score 1215; DB 2; Length 391;  
 Best Local Similarity 72.0%; Pred. No. 2.9e-93;  
 Matches 242; Conservative 31; Mismatches 41; Indels 22; Gaps 4;

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QY 1 MATCIDRCRGNTODDSRRCCKNFPRGFSVNRKIHTHTQIEDDDVWIKMLEAKSDV 60
Db 1 MATCIDRCRGNTODDSRRCCKNFPRGFSVNRKIHTHTQIEDDDVWIKMLEAKSDV 60
QY 45 -----DDVWIKMLEAKSDVKEPILSNVYASTSHRSLESALHILSVKLSNLTNP 115
Db 45 -----DDVWIKMLEAKSDVKEPILSNVYASTSHRSLESALHILSVKLSNLTNP 115
QY 116 LDRDAEVDVWAKIREAKSDIAKEPIVSAYHASTVSRKLEALANTLSVKLSNLTNP 175
Db 116 LDRDAEVDVWAKIREAKSDIAKEPIVSAYHASTVSRKLEALANTLSVKLSNLTNP 175
QY 99 SNTLFEPLFVLESPETIESTKODLIWVKERDPACISYVHCFGLFKAQAHRIAHIT 158
Db 99 SNTLFEPLFVLESPETIESTKODLIWVKERDPACISYVHCFGLFKAQAHRIAHIT 158
QY 176 SNTLFEPLFVLESPETIESTKODLIWVKERDPACISYVHCFGLFKAQAHRIAHIT 235
Db 176 SNTLFEPLFVLESPETIESTKODLIWVKERDPACISYVHCFGLFKAQAHRIAHIT 235
QY 159 LMKONRKRIYALLIONRVSSEFAVDIHPGAKIGKGIILDHATGVVIGFAVGVNDV 218
Db 159 LMKONRKRIYALLIONRVSSEFAVDIHPGAKIGKGIILDHATGVVIGFAVGVNDV 218
QY 219 VTLGGTGKSGDRHPRKIGDVLIGAGSIIIGNITIGGAKIGSGSVVVKDVPARTTAV 278
Db 219 VTLGGTGKSGDRHPRKIGDVLIGAGSIIIGNITIGGAKIGSGSVVVKDVPARTTAV 278
QY 296 VTLGGTGKSGDRHPRKIGDVLIGAGSIIIGNITIGGAKIGSGSVVVKDVPARTTAV 355
Db 296 VTLGGTGKSGDRHPRKIGDVLIGAGSIIIGNITIGGAKIGSGSVVVKDVPARTTAV 355
QY 279 PARLIGKKNPKRKHDPICLTMDOTSYLTEMSDYVI 314
Db 279 PARLIGKKNPKRKHDPICLTMDOTSYLTEMSDYVI 314
QY 356 PARLIGKKNPKRKHDPICLTMDOTSYLTEMSDYVI 391
Db 356 PARLIGKKNPKRKHDPICLTMDOTSYLTEMSDYVI 391

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RESULT 4 S68469

serine O-acetyltransferase (EC 2.3.1.30) sata - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 05-May-2000  
 C:Accession: S68469  
 R:Bogdanova, N.; Bork, C.; Hell, R.  
 FEBS Lett. 358, 43-47, 1995  
 A:Title: Cysteine biosynthesis in plants: isolation and functional identification of  
 A:Reference number: S68469; MUID:95121457  
 A:Accession: S68469  
 A:Molecule type: mRNA  
 A:Residues: 1-303 <BOG>  
 A:Cross-references: EMBL:X82888  
 C:Genetics:  
 A:Gene: sata  
 C:Superfamily: serine acetyltransferase; serine acetyltransferase homology  
 C:Keywords: acyltransferase; coenzyme A; cysteine biosynthesis  
 F:113-272/Domain: serine acetyltransferase homology <SAT>

Query Match 67.3%; Score 1105; DB 2; Length 303;  
 Best Local Similarity 73.0%; Pred. No. 2.8e-84;  
 Matches 222; Conservative 30; Mismatches 36; Indels 16; Gaps 6;

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QY 25 NFRF-PGFS-----VNRKIHTHTQIEDDDVWIKMLEAKSDVKEPILSNVY 71
Db 25 NFRF-PGFS-----VNRKIHTHTQIEDDDVWIKMLEAKSDVKEPILSNVY 71
QY 72 ASITSHRSLESALHILSVKLSNLTNPNTLFEPLFVLESPETIESTKODLIWVKERD 131
Db 72 ASITSHRSLESALHILSVKLSNLTNPNTLFEPLFVLESPETIESTKODLIWVKERD 131
QY 62 ASIVSQRSLEALANTLSVKLSNLTNPNTLFEPLFVLESPETIESTKODLIWVKERD 121
Db 62 ASIVSQRSLEALANTLSVKLSNLTNPNTLFEPLFVLESPETIESTKODLIWVKERD 121
QY 132 PACISYVHCFGLFKAQAHRIAHITLTKONRKRIYALLIONRVSSEFAVDIHPGAKIG 191
Db 132 PACISYVHCFGLFKAQAHRIAHITLTKONRKRIYALLIONRVSSEFAVDIHPGAKIG 191
QY 122 PACISYVHCFGLFKAQAHRIAHITLTKONRKRIYALLIONRVSSEFAVDIHPGAKIG 181
Db 122 PACISYVHCFGLFKAQAHRIAHITLTKONRKRIYALLIONRVSSEFAVDIHPGAKIG 181

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QY 192 GIL-LDHATGCVTIGFAVYGVNDVNSILHGVTLGGTCKGSDGDRPHKIGDGLVLLGAGSCILGN 250
      ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 182 GIFALPHATIAVIGTFAVYGVNNVSIILHNTLTGGTCKGSDGDRPHKIGDGYLL--GTCLIGN 239

QY 251 ITTIGEGAKTIGSGSVVVKDVPARTTAVGNPARLIGKENPRKHDKIPCLTMDQTSYLEWS 310
      ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 240 ITTIGEGAKTIGSGSVLKEVPGGTTVYGNPARLLGGGDNPKTKHDKIPGLTMDQTSIHEWS 299

QY 311 DYVI 314
      ||||
Db 300 DYVI 303

RESULT 5
T09140
serine O-acetyltransferase (EC 2.3.1.30) - spinach
N:Alternate names: serine acetyltransferase
C:Species: Spinacia oleracea (spinach)
C:date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
C:Accession: T09140
R:Saito, K.; Takagi, Y.
submitted to the EMBL Data Library, October 1996
A:Description: A cDNA encoding serine acetyltransferase from spinach.
A:Reference number: Z15582
A:Accession: T09140
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-347 <SAIT>
A:Cross-References: EMBL:D88529
A:Experimental source: Leaf
C:Function:
A:Description: catalyzes conversion of L-serine to O-acetyl serine (by acetyl CoA)
A:Pathway: cysteine biosynthesis
C:Superfamily: serine acetyltransferase; serine acetyltransferase homology
C:Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F:156-316/Domain: serine acetyltransferase homology <SAT>

Query Match 53.4%; Score 877; Db 2; Length 347;
Best Local Similarity 56.6%; Pred. No. 2.9e-65;
Matches 163; Conservative 53; Mismatches 70; Indels 2; Gaps 1;

QY 29 PG--FSVNRKRIHHTQIEDDDVIMKLEAKSDVKQEPILSNYYASTSHRSLESALAH 86
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 60 PGGDLSVAVSAGHLTANNAMWLMQIKGEARDADSEPALASYLTSTLSSLSERLSF 119

QY 87 ILVKLSNLMPLPSNTLFEFLISYLEBSPETIESTQDILAKERDPACISVHCFELFGK 146
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 120 HLGCGLCCSTLSTLLDYDLFNLNLSDDSLDPAVVAADRAARVROPACVPSHCLLNKKG 179

QY 147 FLACQARIHATLMKONRKIVALLIONRVSESAVDIHFGAKTIGKILLDHATGVIGET 206
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 180 FLACQSHRAVHKLMNODRRPLALALHSRISDVFNADIHAAKILGILLFDHATGVIGET 239

QY 207 AVVDNVSILHGVTLGGTCKGSDGDRPHKIGDGYLLGAGSCILGNTTIGEGAKTIGSGSVYV 266
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 240 AIIIDNCSIIHNTLTGGTCKAGDRPHKYGDDGYLLIGAGATIIIGNVRIGDGAKTIGAGSVVL 299

QY 267 KDVPARTTAVGNPARLIGKENPRKHDKIPCLTMDQTSYLEWSDYVI 314
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 300 IDVPRRTTAVGNPARLIGKEKPSQNSDVPGESMDHTFSISEMSDYII 347

RESULT 6
A57478
serine O-acetyltransferase (EC 2.3.1.30) - watermelon
C:Species: Citrullus lanatus (watermelon)
C:date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 20-Jun-2000
C:Accession: A57478
R:Saito, K.; Yokoyama, H.; Noji, M.; Murakoshi, I.
J. Biol. Chem. 270, 16321-16326, 1995
A:Title: Molecular cloning and characterization of a plant serine acetyltransferase play
A:Reference number: A57478; MUID:95332343

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A:Accession: A57478  
A:Status: preliminary: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-294 <SAT>  
A:Cross-references: GB:D49535; NID:g1060871; PIDN:AA08479.1; PID:g1841312  
C:Superfamily: serine acetyltransferase; serine acetyltransferase homology  
C:Keywords: acyltransferase; coenzyme A  
F:103-263/Domain: serine acetyltransferase homology <SAT>

Query Match 53.0%; Score 869; DB 2; Length 294;  
Best Local Similarity 58.6%; Pred. No. 1,1e-64;  
Matches 163; Conservative 49; Mismatches 9; Indels 0; Gaps 0;

37 IHHTDEDDDDVWIKMLEEAKSDVKQEPILSNYYASTSISLESALHLISVLSLN 96  
17 VESTINNDFTWLMGQIKAEARDAESEPALSYLSTLISLSERSISFHLGNLCST 76  
97 LPSNLTLEFLFVLESPELLESTKODLIAVERDPACISVHCELGKFLACQAHRIA 156  
77 LSTLLYDLEFLAFTDYCLRSAAVADLQAEKRPACISVHCLLNKGLACQAHRYA 136  
157 HTLMKONRKIVALLIONRSESFAVDIHPGAKIGKILLATGVIGETAVGVNSIL 216  
137 HKLMNOSRRPLALALOSRIADYPAVDIHPAARIKGILHATGVVGETAVIGNSVL 196  
217 HGVTLGGTGKQSDRHPKIGDGYLIAGSCILGNTTIGCAKIGSGSVVKKVPRTTAV 276  
197 HHVTLGGTGKMGCDRHPKIGDGYLIAGATILLGNVIGCVVIGAGSVVLDIVPRITAV 256  
277 GNPARKLGKKNRPKRKHDKIPCLTMDQTSYLTSEMSDVI 311  
257 GNPARKLVGKEKPSQLEDIPGSEMDHTSFISEMSDYII 211

RESULT 7  
S71207  
serine O-acetyltransferase (EC 2.3.1.30) Sat-52 - A. abdlopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress).  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 05-May-2000  
R:Howatch, J.R.; Roberts, M.A.; Way, J.L.  
C:Accession: S71207  
submitted to the EMBL Data Library, June 1995  
A:Description: Cysteine biosynthesis in higher plants: a novel cDNA clone for serine  
A:Accession: S71207  
A:Molecule type: mRNA  
A:Residues: 1-312 <HOM>  
A:Cross-references: EMBL:U030298; NID:g905390; PIDN:AA049655.1; PID:g905391  
C:Superfamily: serine acetyltransferase; serine acetyltransferase homology  
C:Keywords: acyltransferase; coenzyme A; cysteine biosynthesis  
F:120-280/Domain: serine acetyltransferase homology <SAT>

Query Match 51.8%; Score 849.5; DB 2; Length 312;  
Best Local Similarity 59.7%; Pred. No. 4.9e-64;  
Matches 160; Conservative 45; Mismatches 12; Indels 1; Gaps 1;

48 WTKMKLEEKSVKQEPILSNYYASITSHSLESALAHISVKLSLNIDPSNLTLEFLI 107  
45 LMTQIKAEARRDAEPALASLYSTIHSLSERSISPHGNKLCSTLSTLLYDLEFL 104  
108 SVLESPELLESTKODLIAVERDPACISVHCELGKFLACQAHRIATHLMKONRKIV 167  
105 NFESSPRLNRTAVDLRAARVRDPACISFSCLLNTYKFLAIQAHRSVHKLMQSKRP 164  
168 ALLIQNRVESPAVDIHPPAKIGKGLLDHAAGVYIGETAVGVNSILHGVTLGGTQK 227  
165 ALAHNRISIDYPAVDIHPPAKIGKGLLDHAAGVYIGETAVGVNSILHGVTLGGTGA 224  
228 SGDRHKKIGDGVLIAGSCILGNTTIGCAKIGSGSVVKKVPRTTAVGNPARKLGKE 287  
225 CGDRHKKIGDGVLIAGSCILGNTTIGCAKIGSGSVVKKVPRTTAVGNPARKLGKE 284

QY 288 NPRKHD-KIPCLMOTSYLTWMSDYVI 314  
 Db 285 KPIIHDECPGSMHTSFISEMSDYII 312

## RESULT 8

probable serine O-acetyltransferase [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: F84554

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;

Neus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; MUID:20083487

A:Accession: F84554

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-315 <STO>

A:Cross-references: GB:AE002093; NID:96598796; PIDN:AAF18673.1; GSPDB:GNO0139

C:Genetics:

A:Gene: At3g17640

A:Map position: 2

Query Match

Best Local Similarity 42.6%; Score 699; DB 2; Length 315;

Matches 141; Conservative 50; Mismatches 76; Indels 14; Gaps 4;

QY 27 FRGEFSNRR-IHHTQEDD-----DVIWKMLEAKSDVKOEPLTSNYYASTSHRS 79

Db 8 FESGFEYVAGTKHSESDSNLDPKSDPIWDAIREAK--LEKEPIISFLVAGLHADC 65

QY 80 LESALHILSVKLSNLTNSLTFELFISVLESPELLESTMODLIANKERPACISVH 139

Db 66 LEQALGFVLNRLQNPFLATQOLDFFYGVMMHDKQSSISRHDIQAKRDRPACTSYSS 125

QY 140 CFIQFGFGLACQAHRIAHFLMKONRKIVALLIQNRSSEFAVDIHGAKIGKIGILLDHAT 199

Db 126 AILHLKGYHNLAYRVAHKLWNEGRKLLALQSRISSEFGIDIHPARIEGILLDHGT 185

QY 200 GVVGSTAVAGDNVSLIHGVTGSGKOSGDHPRKIGGVILGAGSCLNITTEGAKI 259

Db 186 GVVGSTAVAGDNVSLIHGVTGSGKOSGDHPRKIGGVILGAGSCLNITTEGAKI 259

QY 260 GSGSVVAVDVPARTAVGNPARLIGKKNPRKHDKIPCLITM 300

Db 246 AAGSLVLKDVPSHVSAGNPALKIRVME-----EQDPSLAM 281

## RESULT 9

probable serine O-acetyltransferase (EC 2.3.1.30) NMA0742 [imported] - Neisseria meningitidis

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 02-Feb-2001

C:Accession: C81184

R:Kettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

ti, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiarant, V.; Pizsa, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; VE

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:2015755

A:Accession: C81184

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-272 <TEI>

A:Cross-references: GB:AE002412; GB:AE002098; NID:97225783; PIDN:AAF40988.1; PID:9722578

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491

A:Reference number: A81775; MUID:20222556

A:Accession: H81917

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-272 <PAR>

A:Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CA884026.1; PID:9737

A:Experimental source: serogroup A, strain 22491

C:Genetics:

A:Gene: cyse; NMB0560; NMA0742

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

C:Keywords: acyltransferase; coenzyme A

F:88-248/Domain: serine acetyltransferase homology <SAT>

Query Match

Best Local Similarity 39.6%; Score 649.5; DB 2; Length 272;

Matches 136; Conservative 39; Mismatches 86; Indels 7; Gaps 2;

QY 47 DVIWKMLEAKSDVKOEPLTSNYYASTSHRSLEBALHILSVKLSNLTNSLTFELF 106

Db 12 DVIWKMLEAKSDVKOEPLTSNYYASTSHRSLEBALHILSVKLSNLTNSLTFELF 106

QY 107 ISVLESPELLESTMODLIANKERPACISVH 139

Db 72 QALGSPDTQIGKCEVADLKAIRYEDPACDEYSLPLIFKCFALDHNHNLHLYDGRKT 131

QY 167 VALLIONRSEFAVDIHGAKIGKIGILLDHATGVIGSTAVAGDNVSLIHGVTGSGK 226

Db 132 LAFLQNRSEFAVDIHGAKIGKIGILLDHATGVIGSTAVAGDNVSLIHGVTGSGK 226

QY 227 QSDGRHPRKIGDGLVILGAGSCLNITTEGAKIGSGSVVAVDVPARTAVGNPARLIGK 286

Db 192 EGSDGRHPRKIGDGLVILGAGSCLNITTEGAKIGSGSVVAVDVPARTAVGNPARLIGK 286

QY 287 ENRKHDKIPCLITMOTSYLTWMSDYVI 314

Db 250 ----KSLKTPSADMDONIQFTF-IDFMI 272

RESULT 10

serine O-acetyltransferase (EC 2.3.1.30) - Escherichia coli

C:Species: Escherichia coli

C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 05-May-2000

C:Accession: A27896; A34563; S47828; A65161

R:Denk, D.; Bock, A.

J. Gen. Microbiol. 133, 515-525, 1987

A:Title: L-Cysteine biosynthesis in Escherichia coli: nucleotide sequence and express

A:Reference number: A27896; MUID:88009872

A:Accession: A27896

A:Molecule type: DNA

A:Residues: 1-273 <DEN>

A:Cross-references: GB:M15745; NID:9145675; PIDN:AAA23648.1; PID:9145676

R:Tel, H.; Murata, K.; Kimura, A.

Biochem. Biophys. Res. Commun. 167, 948-955, 1990

A:Title: Structure and expression of CysX, the second gene in the Escherichia coli K-

A:Accession: A34563

A:Molecule type: DNA

A:Residues: 1-273 <PIU>

A:Cross-references: EMBL:000039; NID:9466582; PIDN:AA818584.1; PID:9466745

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.; Rose, D.J.; Mau, B.; Shao, Y.

64 REVEEAYADPEMIA S A C D I O A V R T B P A Y D K Y S T B L Y I K E H A I O A V B I C H E U T E N I V 1 0 0

A; Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*

area

